Figure 1

DSP-12, 1656 Base Pairs

AAGCAGTGGTAACAACGCAGAGTACGCGGGCGAGGAGAATATCTTGCTGGGAGTGGACT
TTTCCAGTAAGGAAAGTAAAAGCTGCACCATTGGG**ATG**GTTCTCCGACTGTGGAGCGAC
ACGAAAATCCACCTTGATGGAGATGGTGGGTTCAGCGTGAGCACAGCAGGAAGGATGCA
CATATTTAAGCCTGTGTCTGTCCAGGCCATGTGGTCTGCCCTGCAGGTGCTTCACAAGG
CCTGCGAAGTGGCCCGGAGGCACAACTACTTCCCCGGGGGTGTAGCTCTCATCTGGGCT
ACCTACTATGAGAGCTGCATCAGCTCCGAGCAGAGCTGCATCAACGAGTGGAACGCCAT
GCAGGACCTGGAGTCTACGCGGCCCGACTCCCCCGCGCTATTTGTGGACAAGCCCACTG
AAGGGGAAAGGACCGAGCGCCTCATCAAAGCCAAGCTCCGAAGCATCATGATGAGCCAG
GATCTAGAAAATGTGACTTCCAAAGAGATTCGTAATGAATTAGAGAAACAGATGAATTG
TAACTTGAAGGAACTCAAGGAATTTATAGACAATGAGATGCTACTTATCTTGGGACAGA
TGGACAAGCCCTCCCTTATCTTCGATCATCTTTATCTCGGCTCTGAATGGAATGCATCC
AATCTGGAGGAACTGCAGGGCTCAGGGGTTGATTACATTTTAAATGTTACCAGAGAAAT
CGATAATTTTTTTCCTGGCTTATTTGCATATCATAACATCCGAGTCTACGATGAAGAGA
CCACAGACCTCCTCGCCCACTGGAATGAAGCGTATCATTTTATAAACAAAGCGAAGAGG
AACCATTCCAAGTGCCTGGTGCATTGCAAAATGGGCGTGAGTCGCTCGGCCTCCACAGT
CATAGCCTATGCAATGAAGGAATTCGGCTGGCCTCTGGAAAAAGCATATAACTATGTAA
AGCAGAAGCGCAGCATCACGCGCCCCAACGCGGGCTTTATGAGGCAGCTGTCTGAGTAT
GAAGGCATCTTGGATGCAAGCAAACAGCGGCACAACAAGCTGTGGCGTCAGCAGACAGA
CAGCAGCCTCCAGCAGCCTGTGGATGACCCTGCAGGACCTGGCGACTTCTTGCCAGAGA
CCCCAGATGGCACCCCGGAAAGCCAGCTGCCCTTCTTGGATGATGCCGCCCAGCCCGGC
TTAGGGCCCCCCCTCCCCTGCTGTTTCCGGCGACTCTCAGACCCCCTTCTGCCTTCCCC
TGAGGATGAAGCCGGCAGCTTGGTCCACCTGGAGGATCCGGAGAGGGAGGCTCTGTTGG
AGGAAGCTGCTCCACCTGCAGAGGTGCACAGGCCGGCCAGACAGCCCCAGCAAGGTTCC
GGACTCTGTGAGAAGGATGTGAAGAAGAAACTAGAGTTTGGGAGTCCCAAAGGTCGGAG
CGGCTCCTTGCTGCAGGTGGAGGAGACGGAAAGGGAGGAGGGCCTGGGAGCAGGGAGGT
GGGGGCAGCTTCCAACCCAGCTCGATCAAAACCTGCTCAACTCGGAGAACCTAAACAAC
AACAGCAAGAGGAGCTGTCCCAACGGCATGGAGGTAGGCAGAGCCCGGCCTGCAGGGTG
GCACACCCCATCCCTTCCATCCCACTCTAATTGGCCTACCTCAGCCTCTGTAGTAGGGA
CTACAGGCACCCGCCACCACACCCAGCTGATTTTTTTCTATTGTCTCCTCTGGCCCCC
AGCTCCCATCTCCAGGGACCTGAGGGTTCTTTCACAGGG**TGA**TTCTGCTGGTGGGTACG
TAGTGCATACCTTATATAGCAAATTGAGAATCTGTTGGGAATAACACATATCTCTGCAC
ACCATCTTCACCCCATGTACCTTATTCATACCCTGGGCAGGGCTTCCAACTCAATTTCT
TTTTGTGTATGTAAAATTAAAACATATAATTTATCAGCCAAAAAAAAAAAAAAAAAAA
AA

Figure 2

DSP-12, 552 Amino Acids

MVLRLWSDTKIHLDGDGGFSVSTAGRMHIFKPVSVQAMWSALQVLHKACEVARRHNYFP
GGVALIWATYYESCISSEQSCINEWNAMQDLESTRPDSPALFVDKPTEGERTERLIKAK
LRSIMMSQDLENVTSKEIRNELEKQMNCNLKELKEFIDNEMLLILGQMDKPSLIFDHLY
LGSEWNASNLEELQGSGVDYILNVTREIDNFFPGLFAYHNIRVYDEETTDLLAHWNEAY
HFINKAKRNHSKCL**VHCKMGVSRS**ASTVIAYAMKEFGWPLEKAYNYVKQKRSITRPNAG
FMRQLSEYEGILDASKQRHNKLWRQQTDSSLQQPVDDPAGPGDFLPETPDGTPESQLPF
LDDAAQPGLGPPLPCCFRRLSDPLLPSPEDEAGSLVHLEDPEREALLEEAAPPAEVHRP
ARQPQQGSGLCEKDVKKKLEFGSPKGRSGSLLQVEETEREEGLGAGRWGQLPTQLDQNL
LNSENLNNNSKRSCPNGMEVGRARPAGWHTPSLPSHSNWPTSASVVGTTGTRHHTQLIF
FYCLLWAPSSHLQGPEGSFTG

Figure 3

DSP-13, 1527 Base Pairs

CCTGGGAAGAAGTTATCTATCTCTCGAGTGACATTCAAGATATACCGTACCCCTCGGTTCTGTA
AGTCCTCTAAGTTGGAGGCATTCCATTCTGAGCCGGCCCC**ATG**ACCCTGAGCACGTTGGCCCGC
AAGAGGAAGGCGCCCCTCGCTTGCACCTGCAGCCTCGGTGGCCCCGACATGATTCCTTACTTCT
CCGCCAACGCGGTCATCTCGCAGAACGCCATCAACCAGCTCATCAGCGAGAGCTTTCTAACTGT
CAAAGGTGCTGCCCTTTTTCTACCACGGGAAATGGCTCATCCACACCAAGAATCAGCCACAGA
CGGAACAAGCATGCAGGCGATCTCCAACAGCATCTCCAAGCAATGTTCATTTTACTCCGCCCAG
AAGACAACATCAGGCTGGCTGTAAGACTGGAAAGTACTTACCAGAATCGAACACGCTATATGGT
AGTGGTTTCAACTAATGGTAGACAAGACACTGAAGAAAGCATCGTCCTAGGAATGGATTTCTCC
TCTAATGACAGTAGCACTTGTACCATGGGCTTAGTTTTGCCTCTCTGGAGCGACACGCTAATTC
ATTTGGATGGTGATGGTGGGTTCAGTGTATCGACGGATAACAGAGTTCACATATTCAAACCTGT
ATCTGTGCAGGCAATGTGGTCTGCACTACAGAGCTTACACAAGGCTTGTGAAGTCGCCAGAGCG
CATAACTACTACCCAGGCAGCCTATTTCTCACTTGGGTGAGTTATTATGAGAGCCATATCAACT
CAGATCAATCCTCAGTCAATGAATGGAATGCAATGCAAGATGTACAGTCCCACCGGCCCGACTC
TCCAGCTCTCTTCACCGACATACCTACTGAACGTGAACGAACAGAAAGGCTAATTAAAACCAAA
TTAAGGGAGATCATGATGCAGAAGGATTTGGAGAATATTACATCCAAAGAGATAAGAACAGAGT
TGGAAATGCAAATGGTGTGCAACTTGCGGGAATTCAAGGAATTTATAGACAATGAAATGATAGT
GATCCTTGGTCAAATGGATAGCCCTACACAGATATTTGAGCATGTGTTCCTGGGCTCAGAATGG
AATGCCTCCAACTTAGAGGACTTACAGAACCGAGGGGTACGGTATATCTTGAATGTCACTCGAG
AGATAGATAACTTCTTCCCAGGAGTCTTTGAGTATCATAACATTCGGGTATATGATGAAGAGGC
AACGGATCTCCTGGCGTACTGGAATGACACTTACAAATTCATCTCTAAAGCAAAGAAACATGGA
TCTAAATGCCTTGTGCACTGCAAAATGGGGGTGAGTCGCTCAGCCTCCACCGTGATTGCCTATG
CAATGAAGGAATATGGCTGGAATCTGGACCGAGCCTATGACTATGTGAAAGAAAGACGAACGGT
AACCAAGCCCAACCCAAGCTTCATGAGACAACTGGAAGAGTATCAGGGGATCTTGCTGGCAAGC
TTCCTAGGCTTGATTCATGGAGGGAGGGACAAGCCCTGGGGAGAGAAAAGCACAGAATTTGAGT
CAGTAGATCTGGTTTCCATTCCTGGTTCACCCTCTTGCTGCAACCCTGAGAAGTTACTTCACAT
TTCTCATCCTTACCTGACCCCATCTATAAAA**TGA**AAATCAAGAGATCCATCTCACAGGGTTATT
GTGAATAAAAATGTGTTTGAATGTTTATAAAAAAAAAAAAAAAAAAA

Figure 4

DSP-13, 509 Amino Acids

MTLSTLARKRKAPLACTCSLGGPDMIPYFSANAVISQNAINQLISESFLTVKGAALFLPRGNGS
STPRISHRRNKHAGDLQQHLQAMFILLRPEDNIRLAVRLESTYQNRTRYMVVVSTNGRQDTEES
IVLGMDFSSNDSSTCTMGLVLPLWSDTLIHLDGDGGFSVSTDNRVHIFKPVSVQAMWSALQSLH
KACEVARAHNYYPGSLFLTWVSYYESHINSDQSSVNEWNAMQDVQSHRPDSPALFTDIPTERER
TERLIKTKLREIMMQKDLENITSKEIRTELEMQMVCNLREFKEFIDNEMIVILGQMDSPTQIFE
HVFLGSEWNASNLEDLQNRGVRYILNVTREIDNFFPGVFEYHNIRVYDEEATDLLAYWNDTYKF
ISKAKKHGSKCL**VHCKMGVSRS**ASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNPSFMRQLEE
YQGILLASFLGLIHGGRDKPWGEKSTEFESVDLVSIPGSPSCCNPEKLLHISHPYLTPSIK

Figure 5

A DSP13 Alternate Splice Variant, 723 Base Pairs

CTGCCCGGCTTCTAACAGGCCACTGACCGGTACTCACTGGGGACCCACGCTCTAAGTTGTTGAT
CTCTAGAACCGATTTTGGAAAAGGATTTGCCTTATTGAAGAAGACAGGATCATTCTTCTTTCTT
TCCCATTTAAGAATAATCGTTATTAAGAATATCGTTTAAGAATAATCGTTATTTCTCTCTTCTC
AGACCTACTGAACGTGAACGAACAGAAAGGCTAATTAAAACCAAATTAAGGGAGATC**ATG**ATGC
AGAAGGATTTGGAGAATATTACATCCAAAGAGATAAGAACAGAGTTGGAAATGCAAATGGTGTG
CAACTTGCGGGAATTCAAGGAATTTATAGACAATGAAATGATAGTGATCCTTGGTCAAATGGAT
AGCCCTACACAGATATTTGAGCATGTGTTCCTGGGCTCAGAATGGAATGCCTCCAACTTAGAGG
ACTTACAGAACCGAGGGGTACGGTATATCTTGAATGTCACTCGAGAGATAGATAACTTCTTCCC
AGGAGTCTTTGAGTATCATAACATTCGGGTATATGATGAAGAGGCAACGGATCTCCTGGCGTAC
TGGAATGACACTTACAAATTCATCTCTAAAGCAAAGAAACATGGATCTAAATGCCTTGTGCACT
GCAAAATGGGGGTGAGTCGCTCAGCCTCCACCGTGATTGCCTATGCAATGAAGGAATATGGCTG
GAATCTGGACCGAGCCTATGACTATGTGAAAGAAAGACGAACGGTAACCAAGCCCAACCCAAGC
TTCATGAGACAACTGGAAGAGTATCAGGGGATCTTGCTGGCAAGCTTCCTAGGCTTGATTCATG
GAGGGAGGGACAAGCCCTGGGGAGAGAAAAGCACAGAATTTGAGTCAGTAGATCTGGTTTCCAT
TCCTGGTTCACCCTCTTGCTGCAACCCTGAGAAGTTACTTCACATTTCTCATCCTTACCTGACC
CCATCTATAAAA**TGA**AAATCAAGAGATCCATCTCACAGGGTTATTGTGAATAAAAATGTGTTTG
AATGTTTATAAAAAAAAAAAAAAAAAAA

B DSP13 Alternate Splice Variant, 241 Amino Acids

MMQKDLENITSKEIRTELEMQMVCNLREFKEFIDNEMIVILGQMDSPTQIFEHVFLGSEWNASN
LEDLQNRGVRYILNVTREIDNFFPGVFEYHNIRVYDEEATDLLAYWNDTYKFISKAKKHGSKCL
VHCKMGVSRSASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNPSFMRQLEEYQGILLASFLGL
IHGGRDKPWGEKSTEFESVDLVSIPGSPSCCNPEKLLHISHPYLTPSIK

```
          1       10        20        30        40        50        60        70        80        90       100
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
    PYST1   SDLDRD-PNSATDSDGSPLSNSQPSFPVEILPFLYLGCAKDSTNLDVLEEFGIKYILNVTP-------NLPNLFENAGEFKYKQIPISDHWSQNLSQF
    MKP-7      DRELPSSATESDGSPVPSSQPAFPVQILPYLYLGCAKDSTNLDVLGKYGIKYILNVTP-------NLPNAFEHGGEFTYKQIPISDHWSQNLSQF
   MKP-4,                GATPPPVGLRASFPVQILPNLYLGSARDSANLESLAKLGIRYILNVTP-------NLPNFFEKNGDFHYKQIPISDHWSQNLSRF
     hVH5   GLCEGKPAALLPHSLSQPCLPVPSVGLTRILPHLYLGSQKDVLNKDLMTQNGISYVLNASN-------SCPKP-DFICESRFMRVPINDNYCEKLLPW
     PAC1   PAQALPPAGAENSNSDPRVPIYDQGGPVEILPYLYLGSCNHSSDLQGLQACGITAVLNVSA-------SCPNHFE--GLFHYKSIPVEDNQMVEISAW
    MKP-1   PLSTSVPDSAESGCSSCSTPLYDQGGPVEILPFLYLGSAYHASRKDMLDALGITALINVSA-------NCPNHFE--GHYQYKSIPVEDNHKADISSW
   MKP-2,   PVPPSATEPLDLGCSSCGTPLHDQGGPVEILPFLYLGSAYHAARRDHLDALGITALLNVSS-------DCPNHFE--GHYQYKCIPVEDNHKADISSW
    MKP-5   SERALISQCGKPVVNVSYRPAYDQGGPVEILPFLYLGSAYHASKCEFLANLHITALLNVSR-------RTSEACM--THLHYKWIPVEDSHTADISSH
   DSP-12   QMNCNLKELKEFIDNEMLLILGQMDKPSLIFDHLYLGSEWNASNLEELQGSGVDYILNVTR-------EIDNFFP--GLFAYHNIRVYDEETTDLLAH
   DSP-13   QMVCNLREFKEFIDNEHIVILGQMDSPTQIFEHVFLGSEWNASNLEDLQNRGVRYILNVTR-------EIDNFFP--GVFEYHNIRVYDEEATDLLAY
      VHR SGSFELSVQDLNDLLSDGSGCYSLPSQPCNEVTPRIYVGNASVAQDIPKLQKLGITHVLNAAEGRSFMHVNTWANFYKDSGITYLGIKANDTQEFNLSAY
Consensus                             p e!lp lY1Gsa  a n   $   g! y LNv           pn f   g   %  !p  D     ls

          101    110       120       130       140       150       160       170       18082
          |--------+---------+---------+---------+---------+---------+---------+---------+-|
    PYST1 FPEAISFIDEA-RGKNCGVLVHCLAGISRSVTVTVAYLMQKLNLSMNDAYDIVKMKKSNISPNFNFMGQLLDFERTLGLSS
    MKP-7 FPEAISFIDEA-RSKKCGVLVHCLAGISRSVTVTVAYLMQKMNLSLNDAYDFVKRKKSNISPNFNFMGQLLDFERTLGLSS
   MKP-4, FPEAIEFIDEA-LSQNCGVLVHCLAGVSRSVTVTVAYLMQKLHLSLNDAYDLVKRKKSNISPNFNFMGQLLDFERSLRLE
     hVH5 LDKSIEFIDKA-KLSSCQVIVHCLAGISRSATIAIAYIMKTMGMSSDDAYRFVKDRRPSISPNFNFLGQLLEYERTLKLLA
     PAC1 FQEAISFIDSV-KNSGGRVLVHCQAGISRSATICLAYLIQSHRVRLDEAFDFVKQRRGVISPNFSFMGQLLQLETQVLCH
    MKP-1 FNEAIDFIDSI-KNAGGRVFVHCQAGISRSATICLAYLMRTNRVKLDEAFEFVKQRRSIISPNFSFMGQLLQFESQVLAPH
   MKP-2, FMEAIEYIDAV-KDCRGRVLVHCQAGISRSATICLAYLMMKKRVRLEEAFEFVKQRRSIISPNFSFMGQLLQFESQVLATS
    MKP-5 FQEAIDFIDCV-REKGGKVLVHCEAGISRSPTICMAYLMKTKQFRLKEAFDYIKQRRSMVSPNFGFMGQLLQYESEILPSTP
   DSP-12 WNEAYHFINKA-KRNHSKCLVHCKMGVSRSASTVIAYAMKEFGWPLEKAYNYVKQKRSITRPNAGFMRQLSEYEGILDASKQ
   DSP-13 WNDTYKFISKA-KKHGSKCLVHCKMGVSRSASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNPSFMRQLEEYQGILLASFL
      VHR FERAADFIDQALAQKNGRVLVHCREGYSRSPTLVIAYLMNRQKMDVKSALSIVRQNRE-IGPNDGFLAQLCQLNDRLAKEG
Consensus f eai FI# a k     vlVHC aGiSRSat  iAYlM      l  Ay  !kqrr  isPNf F$gQLl# #  l
```

Figure 6

Alignment of DSP-12 and DSP-13

```
         1        10        20        30        40        50        60        70        80        90        100       110
         |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
DSP-13   MTLSTLARKRKAPLACTCSLGGPDMIPYFSANAVISQNAINQLISESFLTVKGAALFLPRGNGSSTPRISHRRNKHAGDLQQHLQAMFILLRPEDNIRLAVRLESTYQNR

         111      120       130       140       150       160       170       180       190       200       210       220
         |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
DSP-12                                       MVLRLWSDTKIHLDGDGGFSVSTAGRMHIFKPVSVQAMWSALQVLHKACEVARRHNYFPGGVALIWATYYESCI
DSP-13   TRYMVVVSTNGRQDTLESIVLGMDFSSNDSSTCTMGLVLPLWSDTLIHLDGDGGFSVSTDNRVHIFKPVSVQAMWSALQSLHKACEVARAHNYYPGSLFLTWVSYYESHI

         221      230       240       250       260       270       280       290       300       310       320       330
         |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
DSP-12   SSEQSCINEWNAMQD ESTRPDSPALFVDKPTEGERTERLIKAKLRSIMNSQDLENVTSKEIRNELEKQMNCNLKELKEFIDNEMLLILGQMDKPSLIFDHLYLGSEWNA
DSP-13   NSDQSSVNEWNAMQDVQSHRPDSPALFTDIPTERERTERLIKTKLREIMMQKDLENITSKEIRTELEMQHVCNLREFKEFIDNEMIVILGQMDSPTQIFEHVFLGSEWNA

         331      340       350       360       370       380       390       400       410       420       430       440
         |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
DSP-12   SNLEELQGSGVDYIL HVTREIDNFFPGLFAYHNIRVYDEETTDLLAHWNEAYHFINKAKRNHSKCLVHCKMGVSRSASTVIAYAMKEFGWPLEKAYNYVKQKRSITRPNA
DSP-13   SNLEDLQNRGVRYILHVTREIDNFFPGVFEYHNIRVYDEEATDLLAYWNDIYKFISKAKKHGSKCLVHCKMGVSRSASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNP

         441      450       460       470       480       490       500       510       520       530       540       550
         |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
DSP-12   GFMRQLSEYEGILDHSKQR--HNKLWRQQTDSSLQ-QPVDDPAGPGDFLPETPDGTPESQLPFLDDAAQPGLGPPLPCCFRRLSDPLLPSPEDEAGSLVHLEDPEREALL
DSP-13   SFMRQLEEYQGILLHSFLGLIHGGRDKPWGEKSTEFESVDLVSIPGSPSCCNPEKLLHISHPYLTPSIK

         551      560       570       580       590       600       610       620       630       640       650       660
         |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
DSP-12   EEAAPPAEVHRPARQPQQGSGLCEKDVKKKLEFGSPKGRSGSLLQVEETEREEGLGAGRWGQLPTQLDQNLLNSENLNNNSKRSCPNGMEVGRARPAGWHTPSLPSHSNW

         661      670       680       690       701
         |---------+---------+---------+----------+|
DSP-12   PTSASVVGTIGTRHITQLIFFYCLLWAPSSHLQGPEGSFTG
```

Figure 7